001560-377.ST25

SEQUENCE LISTING

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<120>   GENE ENCODING PROTEIN HAVING AURONE SYNTHESIZING ACTIVITY

<130>   001560-377

<140>   US 09/446,089
<141>   1999-12-17

<150>   PCT/JP99/02045
<151>   1999-04-16

<150>   JP 10/107296
<151>   1998-04-17

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<170>   PatentIn version 3.0

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<222>   (96)..(1781)

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gttgtttatt atcaatcaaa taaaattatt tccca atg ttc aaa aat cct aat   113
                                        Met Phe Lys Asn Pro Asn
                                        1   5

atc cgc tat cac aaa cta tct tcc aaa tcc aat gac aac gat caa gaa   161
Ile Arg Tyr His Lys Leu Ser Ser Lys Ser Asn Asp Asn Asp Gln Glu
            10   15   20

tcc tcc cat cgt tgt aag cac att cta tta ttt ata ata acc tta ttc   209
Ser Ser His Arg Cys Lys His Ile Leu Leu Phe Ile Ile Thr Leu Phe
        25   30   35

cta ctt ata gtt ggc ctg tac atc gcc aac tct ctc gcc tat gcc cgg   257
Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn Ser Leu Ala Tyr Ala Arg
    40   45   50

ttt gcc tcg acc tca acc ggc cct atc gcc gcc cct gat gtc acc aaa   305
Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala Ala Pro Asp Val Thr Lys

```
       55                      60                      65                      70
tgt ggt cag cca gac ttg cca cct ggc aca gcc cca ata aac tgt tgt        353
Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr Ala Pro Ile Asn Cys Cys
            75                  80                  85

ccc cca atc ccc gct aaa atc atc gat ttc gag cta cca cct ccc tcc        401
Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe Glu Leu Pro Pro Pro Ser
            90                  95                  100

act acc atg agg gtt cgc cgt gcg gct cat tta gtt gat gat gca tac        449
Thr Thr Met Arg Val Arg Arg Ala Ala His Leu Val Asp Asp Ala Tyr
            105                 110                 115

att gcc aaa ttc aag aaa gcc gtt gag ctt atg cga gct cta cct gag        497
Ile Ala Lys Phe Lys Lys Ala Val Glu Leu Met Arg Ala Leu Pro Glu
            120                 125                 130

gat gac cct cgt agc ttc aag caa caa gct aac gtc cat tgc gct tac        545
Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala Asn Val His Cys Ala Tyr
135                 140                 145                 150

tgc gcg ggg gcg tat aat caa gcc ggt ttc aca aac cta aag ctc caa        593
Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe Thr Asn Leu Lys Leu Gln
                155                 160                 165

atc cac cga tct tgg ctt ttt ttc ccg ttc cat aga tat tat atc tac        641
Ile His Arg Ser Trp Leu Phe Phe Pro Phe His Arg Tyr Tyr Ile Tyr
                170                 175                 180

ttt ttt gaa aga ata ttg gga aaa cta atc aat gat aca act ttt gct        689
Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile Asn Asp Thr Thr Phe Ala
            185                 190                 195

ctc caa ttt tgg aac tat gat tca cct ggt gga atg aca atc cca tca        737
Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly Gly Met Thr Ile Pro Ser
            200                 205                 210

atg ttt att gat act aat tct tcg ctg tac gat agt tta cgg gac agt        785
Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr Asp Ser Leu Arg Asp Ser
215                 220                 225                 230

aat cat cag cca cca acc atc gta gac ttg aac tac gcc ttt tct gat        833
Asn His Gln Pro Pro Thr Ile Val Asp Leu Asn Tyr Ala Phe Ser Asp
                235                 240                 245

tcc gac aat acc act act cct gaa gag caa atg att ata aac ctt aaa        881
Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln Met Ile Ile Asn Leu Lys
            250                 255                 260

att gtg tac aga caa atg gtg tcg agc gct aag act cca cag ctt ttc        929
Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe
            265                 270                 275

ttc ggc cgc cca tac cga cgt ggg gac caa gag ttt ccc ggg gtg ggg        977
Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly
            280                 285                 290
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tcg att gag tta gtc cct cat ggc atg ata cat tta tgg acc ggt tct    1025
Ser Ile Glu Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser
295                 300             305                 310

gag aac acg ccc tat ggc gag aac atg ggg gct ttc tac tca acg gct    1073
Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala
                315             320                 325

aga gac ccg ata ttt ttt gct cat cat tcg aac gtc gat aga atg tgg    1121
Arg Asp Pro Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp
                330             335                 340

tcc ata tgg aag acc cta gga ggg ccg cgg agg acg gac tta aca gat    1169
Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp
            345             350             355

cca gat ttt ctt gat gcg tct ttc gtt ttt tat gac gaa aac gca gag    1217
Pro Asp Phe Leu Asp Ala Ser Phe Val Phe Tyr Asp Glu Asn Ala Glu
    360             365             370

atg gtt cgg gtc aag gtt cgg gat tgc tta gat gaa aag aaa cta ggg    1265
Met Val Arg Val Lys Val Arg Asp Cys Leu Asp Glu Lys Lys Leu Gly
375                 380             385                 390

tac gtt tat caa gat gtg gag att ccg tgg ctc aac act cgt cca aca    1313
Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp Leu Asn Thr Arg Pro Thr
                395             400                 405

cca aaa gtt tct ccg tct cta ctt aag aaa ttt cat aga aca aac act    1361
Pro Lys Val Ser Pro Ser Leu Leu Lys Lys Phe His Arg Thr Asn Thr
                410             415                 420

gcc aat ccg aga caa gtt ttt cct gcg ata ctt gac aga gtc tta aaa    1409
Ala Asn Pro Arg Gln Val Phe Pro Ala Ile Leu Asp Arg Val Leu Lys
            425             430             435

gtt atc gtg acg agg ccg aag aaa act aga agt agg aaa gaa aag gac    1457
Val Ile Val Thr Arg Pro Lys Lys Thr Arg Ser Arg Lys Glu Lys Asp
    440             445             450

gag tta gaa gag att tta gtg att gaa ggg att gaa ctg gaa aga gac    1505
Glu Leu Glu Glu Ile Leu Val Ile Glu Gly Ile Glu Leu Glu Arg Asp
455                 460             465                 470

cac ggg cac gta aaa ttc gac gtt tat att aat gct gac gaa gat gac    1553
His Gly His Val Lys Phe Asp Val Tyr Ile Asn Ala Asp Glu Asp Asp
                475             480                 485

ctt gcg gtg att tcg ccg gag aat gct gag ttc gcc ggg agt ttc gtg    1601
Leu Ala Val Ile Ser Pro Glu Asn Ala Glu Phe Ala Gly Ser Phe Val
            490             495                 500

agt ctg tgg cac aaa cct ata aag ggg aag agg aca aag acg cag tta    1649
Ser Leu Trp His Lys Pro Ile Lys Gly Lys Arg Thr Lys Thr Gln Leu
            505             510             515

tta aca ttg tcg att tgt gat att ttg gag gat ttg gat gct gac gaa    1697
Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu
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Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu Asp Leu Asp Ala Asp Glu
    520                 525                 530

gat gat tat gtg ttg gtc act ttg gtt ccg aga aac gcc gga gat gcg   1745
Asp Asp Tyr Val Leu Val Thr Leu Val Pro Arg Asn Ala Gly Asp Ala
535                 540                 545                 550

atc aag att cat aat gtc aag att gag ctt gat ggc taataaattc        1791
Ile Lys Ile His Asn Val Lys Ile Glu Leu Asp Gly
                555                 560

tattgatttc ttctcaacct acagttgatc atttaccgat tgattattcc aataaaagta  1851

tctcatgtac caatatcgat cgtattaatc gtaatacttt cagattttta tttatttaaa  1911

agcagttgta taaatggtga aataaggatt actttttgag                        1951
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<213> Antirrhinum majus

<400> 2

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Met Phe Lys Asn Pro Asn Ile Arg Tyr His Lys Leu Ser Ser Lys Ser
1               5                   10                  15

Asn Asp Asn Asp Gln Glu Ser Ser His Arg Cys Lys His Ile Leu Leu
            20                  25                  30

Phe Ile Ile Thr Leu Phe Leu Leu Ile Val Gly Leu Tyr Ile Ala Asn
        35                  40                  45

Ser Leu Ala Tyr Ala Arg Phe Ala Ser Thr Ser Thr Gly Pro Ile Ala
    50                  55                  60

Ala Pro Asp Val Thr Lys Cys Gly Gln Pro Asp Leu Pro Pro Gly Thr
65                  70                  75                  80

Ala Pro Ile Asn Cys Cys Pro Pro Ile Pro Ala Lys Ile Ile Asp Phe
                85                  90                  95

Glu Leu Pro Pro Pro Ser Thr Thr Met Arg Val Arg Arg Ala Ala His
            100                 105                 110

Leu Val Asp Asp Ala Tyr Ile Ala Lys Phe Lys Lys Ala Val Glu Leu
            115                 120                 125
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Met Arg Ala Leu Pro Glu Asp Asp Pro Arg Ser Phe Lys Gln Gln Ala
130             135             140

Asn Val His Cys Ala Tyr Cys Ala Gly Ala Tyr Asn Gln Ala Gly Phe
145             150             155             160

Thr Asn Leu Lys Leu Gln Ile His Arg Ser Trp Leu Phe Phe Pro Phe
                165             170             175

His Arg Tyr Tyr Ile Tyr Phe Phe Glu Arg Ile Leu Gly Lys Leu Ile
            180             185             190

Asn Asp Thr Thr Phe Ala Leu Gln Phe Trp Asn Tyr Asp Ser Pro Gly
        195             200             205

Gly Met Thr Ile Pro Ser Met Phe Ile Asp Thr Asn Ser Ser Leu Tyr
210             215             220

Asp Ser Leu Arg Asp Ser Asn His Gln Pro Pro Thr Ile Val Asp Leu
225             230             235             240

Asn Tyr Ala Phe Ser Asp Ser Asp Asn Thr Thr Thr Pro Glu Glu Gln
            245             250             255

Met Ile Ile Asn Leu Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala
            260             265             270

Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
        275             280             285

Glu Phe Pro Gly Val Gly Ser Ile Glu Leu Val Pro His Gly Met Ile
    290             295             300

His Leu Trp Thr Gly Ser Glu Asn Thr Pro Tyr Gly Glu Asn Met Gly
305             310             315             320

Ala Phe Tyr Ser Thr Ala Arg Asp Pro Ile Phe Phe Ala His His Ser
            325             330             335

Asn Val Asp Arg Met Trp Ser Ile Trp Lys Thr Leu Gly Gly Pro Arg
            340             345             350

Arg Thr Asp Leu Thr Asp Pro Asp Phe Leu Asp Ala Ser Phe Val Phe
```

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             355                    360                      365

Tyr Asp Glu Asn Ala Glu Met Val Arg Val Lys Val Arg Asp Cys Leu
    370                 375             380

Asp Glu Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro Trp
385                 390             395                     400

Leu Asn Thr Arg Pro Thr Pro Lys Val Ser Pro Ser Leu Leu Lys Lys
                405             410                 415

Phe His Arg Thr Asn Thr Ala Asn Pro Arg Gln Val Phe Pro Ala Ile
                420             425                 430

Leu Asp Arg Val Leu Lys Val Ile Val Thr Arg Pro Lys Lys Thr Arg
                435             440             445

Ser Arg Lys Glu Lys Asp Glu Leu Glu Glu Ile Leu Val Ile Glu Gly
    450                 455             460

Ile Glu Leu Glu Arg Asp His Gly His Val Lys Phe Asp Val Tyr Ile
465                 470             475                     480

Asn Ala Asp Glu Asp Asp Leu Ala Val Ile Ser Pro Glu Asn Ala Glu
                485             490                 495

Phe Ala Gly Ser Phe Val Ser Leu Trp His Lys Pro Ile Lys Gly Lys
            500             505                 510

Arg Thr Lys Thr Gln Leu Leu Thr Leu Ser Ile Cys Asp Ile Leu Glu
            515             520                 525

Asp Leu Asp Ala Asp Glu Asp Asp Tyr Val Leu Val Thr Leu Val Pro
    530                 535             540

Arg Asn Ala Gly Asp Ala Ile Lys Ile His Asn Val Lys Ile Glu Leu
545                 550             555                     560

Asp Gly


<210>   3
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<212>   PRT
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<213> Antirrhinum majus

<400> 3

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Lys Lys Leu Gly Tyr Val Tyr Gln Asp Val Glu Ile Pro
1               5                   10
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<210> 4
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<213> Antirrhinum majus

<400> 4

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Lys Ile Val Tyr Arg Gln Met Val Ser Ser Ala Lys
1               5                   10
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<210> 5
<211> 18
<212> PRT
<213> Antirrhinum majus

<400> 5

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Lys Thr Pro Gln Leu Phe Phe Gly Arg Pro Tyr Arg Arg Gly Asp Gln
1               5                   10                  15

Glu Phe
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<210> 6
<211> 29
<212> PRT
<213> Antirrhinum majus

<220>
<221> UNSURE
<222> (8)..(8)
<223> Amino acid 8 is Xaa wherein Xaa = unknown or other.

<220>
<221> UNSURE
<222> (28)..(28)
<223> Amino acid 28 is Xaa wherein Xaa = unknown or other.

<400> 6

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Lys Ile Asp Phe Glu Leu Pro Xaa Pro Ser Thr Thr Met Arg Val Arg
1               5                   10                  15

Arg Ala Ala His Leu Val Asp Asp Ala Tyr Ile Xaa Lys
            20                  25
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<210> 7

<211> 125
<212> PRT
<213> Antirrhinum majus

<400> 7

Arg Gln Met Val Ser Ser Ala Lys Thr Pro Gln Leu Phe Phe Gly Arg
1   5   10   15

Pro Tyr Arg Arg Gly Asp Gln Glu Phe Pro Gly Val Gly Ser Ile Glu
            20   25   30

Leu Val Pro His Gly Met Ile His Leu Trp Thr Gly Ser Glu Asn Thr
        35   40   45

Pro Tyr Gly Glu Asn Met Gly Ala Phe Tyr Ser Thr Ala Arg Asp Pro
        50   55   60

Ile Phe Phe Ala His His Ser Asn Val Asp Arg Met Trp Ser Ile Trp
65   70   75   80

Lys Thr Leu Gly Gly Pro Arg Arg Thr Asp Leu Thr Asp Pro Asp Phe
                85   90   95

Leu Asp Ala Ser Phe Val Phe Cys Asp Glu Asn Ala Glu Met Val Arg
            100   105   110

Val Lys Val Arg Asp Cys Leu Asp Gly Lys Lys Leu Gly
        115   120   125

<210> 8
<211> 7
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> PEPTIDE
<222> (2)..(2)
<223> Amino acid 2 is Xaa wherein Xaa = Val or Ile.

<400> 8

Phe Xaa Lys Phe Thr Ala Ile
1   5

<210> 9
<211> 6
<212> PRT
<213> Artificial Sequence

<220>
<223> Primer

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<220>
<221>  PEPTIDE
<222>  (6)..(6)
<223>  Amino acid 6 is Xaa wherein Xaa = Thr or Pro.

<400>  9

Lys Trp Lys Gly Lys Xaa
1               5


<210>  10
<211>  6
<212>  PRT
<213>  Artificial Sequence

<220>
<223>  Primer

<400>  10

His Ala Val Cys Asn Glu
1               5


<210>  11
<211>  20
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer

<220>
<221>  misc_feature
<222>  (6)..(18)
<223>  Nucleotides 6, 15 and 18 are "n" wherein "n" = a or c or g
       or t/u or unknown or other


<400>  11
ttyrtnaart tyacngcnat                                          20


<210>  12
<211>  17
<212>  DNA
<213>  Artificial Sequence

<220>
<223>  Primer

<220>
<221>  misc_feature
<222>  (12)..(12)
<223>  Nucleotide 12 is "n" wherein "n" = a or c or g or t/u
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or unknown or other

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aartggaarg gnaarmc   17

<210> 13
<211> 18
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<220>
<221> misc_feature
<222> (4)..(7)
<223> Nucleotides 4 and 7 are "n" wherein "n" = a or c or g or
      t/u or unknown or other

<400> 13
rtgngcnacr carttytc   18

<210> 14
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 14
aaggatccgg ccctatcgcc   20

<210> 15
<211> 22
<212> DNA
<213> Artificial Sequence

<220>
<223> Primer

<400> 15
gggttcgaag aattcatctc tg   22